Evolution of developmental mechanisms in plants

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As our understanding of developmental mechanisms in flowering plant species has become more advanced, an appreciation of the need to understand how distinct plant morphologies are generated has grown. This has led to an awareness of the key morphological differences in distinct land plant groups and to an assessment of the major innovations that occurred during land plant evolution. Recent advances demonstrate how developmental toolkits have been recruited for related purposes in different land plant groups, but the limited number of examples highlights both the infancy of the field and the difficulty of working with non-flowering plants.

Introduction

Land plants evolved from green algae in the mid-Ordovician, over 450 million years ago [1]. Phylogenetic analyses based on both morphological and molecular data suggest that within the green algae, charophytes in the order Charales are the sister group to the land plants [2]. The cellular innovations that facilitated the transition from growth in water to growth on land include the formation of waxy cuticles on vegetative tissue and the re-localization of sporopollenin deposition from the zygote in charophytes to the spores in land plants. Both of these features are synapomorphies of land plants that enabled reproductive success in a non-aqueous environment by conferring desiccation resistance. Subsequent innovations within different land plant lineages led to the diverse morphologies seen in extant (living) land plant groups. This review outlines our current understanding of the developmental mechanisms underlying those innovations.

Land plant phylogeny

Since the colonization of land, plant form and function have diversified significantly. The extent and nature of the innovations that led to this diversification is most easily seen by comparing extant land plant groups, and by considering the phylogenetic relationships between them. The least controversial phylogenetic distinction is between the bryophytes (liverworts, mosses and hornworts) and the tracheophytes (vascular plants) (Fig. 1). The vascular plants are monophyletic, with seed plants (gymnosperms and angiosperms), monilophytes (ferns and horsetails) and lycophytes each forming monophyletic groups within that clade. By contrast, the more basal bryophytes comprise a paraphyletic grade in which the relationships between each lineage have been difficult to resolve [3,4]. The most recent and most comprehensive analysis of bryophyte relationships resolves the liverworts as the most basal group (and thus sister group to all other land plants), and the hornworts as most likely sister group to the vascular plants [5**].

Developmental innovations during land plant evolution

As land plants evolved, developmental mechanisms were either generated de novo or were recruited from existing toolkits and adapted to facilitate changes in form. Some of these changes occurred once, others on multiple occasions, and others were gained and then subsequently lost in a subset of lineages. The changes that had most influence on the elaboration of form in the diploid sporophyte growth phase are summarized below and depicted in Fig. 2:

- Development of a multi-cellular embryo
  In charophytes, the majority of the life cycle is represented by the haploid gametophyte and only the unicellular zygote is diploid, undergoing meiosis rather mitosis after formation. Embryo development represents a major growth transition in that meiotic division of the zygote is delayed and cells divide by mitosis giving rise to a multi-cellular sporophyte.

- Sporophyte growth from a defined apical cell(s)
  Bryophyte sporophytes all have a single axis of growth that terminates de novo or were recruited from existing sporangia. Liverworts grow from cell divisions throughout the structure, mosses grow from both an apical cell and a basal intercalary meristem and hornworts grow from a basal meristem [6]. By contrast, growth in all vascular plants occurs from an apical cell or cells.

- Branching in the sporophyte
  Whereas bryophytes have unbranched sporophytes that subtend a sporangium, protrachyphyte fossil sporophytes from the Silurian have multiple branches that terminate in sporangia, and are therefore named polysporangiates [7]. Unlike extant polysporangiates,
the protracheophyte fossils Aglaophyton major and Horneophyton lignieri are non-vascular. Therefore, sporophyte branching mechanisms evolved after the divergence of bryophytes and protracheophytes but before the appearance of tracheophytes. From a developmental perspective, this observation is important because it implies that branching evolved before vascularization.

- Development of a vascular system
  Increasingly complex body plans and competition for light led to the evolution of taller plants. As such, the need for mechanical support and for transport of water intensified. Coupled with the origin of lignin in vascular plants, these drivers led to the evolution of lignified conducting cells (tracheids). Whereas moss and some liverwort gametophytes transport water through conducting hydroids comprised of elongated cells with just primary cell walls, and protracheophyte fossils show evidence of a similar system [8], true tracheophytes transport water through xylem cells that have lignified secondary cell walls. Tracheophyte fossils indicate that tracheids first evolved in the mid-Silurian (~420 mya) [9].

- Development of roots.
  Charophyte algae and free-living gametophytes develop root-like structures, but ‘true’ roots are only found in sporophytes of vascular plants. Gametophyte ‘roots’ are of three types: single celled rhizoid-like structures that are analogous to root hairs; multi-cellular rhizoid-like projections from a subterranean rhizome or mycorrhizas formed following a fungal association [10]. Whereas rhizoids provide conduits for water and nutrient transport, only the subterranean rhizomes enhance mechanical support. By contrast, true roots provide both transport capability and mechanical support. By definition they are multi-cellular, have a defined endodermis (with the exception of extant Lycopodium roots), produce lateral organs endogenously and have a root cap. Fossil data support the suggestion that lycophyte and euphyllophyte (monilophyte and seed plant) lineages diverged before roots evolved [10].

- Development of leaves
  The evolution of leaves followed a very similar trajectory to that of roots in that small ‘leaf-like’ structures are present on some extant free-living gametophytes but ‘true’ leaves comprising lignified vasculature and multiple cell layers are only found on sporophytes of vascular plants. Fossil evidence suggests that like roots, sporophyte leaves evolved on at least two separate occasions, once in the lycophytes and once in the euphyllophytes [11].

- Formation of seeds
  Before the evolution of seeds, plants reproduced via spores and fertilization required water because sperm
had to swim. In seed plants, the female gametophyte develops inside a modified and protected megasporangium and the male gametophyte (the pollen grain) develops within the microsporangium. Female and male reproductive organs are borne on condensed and modified branching systems (cones in gymnosperms, and flowers in angiosperms). The evolution of these modifications permitted radiation of the seed plants by allowing dispersal of seed into previously uncolonized dryer habitats.

Development of flowers
The evolution of angiosperm flowers involved the modification of organ fate to produce ovules enclosed in carpels, and pollen enclosed in two pairs of sacs in the stamen. Sepals and petals evolved within the angiosperm lineage and allowed for specialization to attract animal pollinators.

The evolution of developmental mechanisms
Micro-evolutionary versus macro-evolutionary questions
The study of how developmental mechanisms evolved in land plants is still in its infancy. To date, most work has focused on the evolution of flowers, primarily because the genetic basis of floral development is well understood in model organisms and because a number of angiosperm species lend themselves to both forward and reverse genetic manipulations (see [12–14,15] for examples and recent reviews). Although micro-evolutionary questions within the angiosperms are clearly extremely important, an understanding of how novelties in plant architecture evolved demands answers to macro-evolutionary questions. Unfortunately, these questions are rarely tackled despite the land plant phylogeny being well resolved at deep nodes because of the difficulty with which non-flowering plant species can be grown and experimentally manipulated.

Experimental organisms
Within the bryophytes, the most tractable experimental system is the moss *Physcomitrella patens*. Transformation and homologous recombination have been possible for many years with this species, and the genome sequence was completed earlier this year [16]. Whilst *P. patens* has been generally accepted as ‘the’ model moss species, there are currently no equivalent liverwort or hornwort...
species. *Marchantia polymorpha* has been proposed as a model liverwort partly because transformation of the thalloid gametophyte is possible by particle bombardment [17]. However, *M. polymorpha* is not in the most basal liverwort group, and perhaps more importantly for considerations of morphological novelty, *M. polymorpha* is a complex thalloid liverwort, whereas the majority (85%) of liverwort species are leafy/simple thalloid forms [18]. *Anthoceros formosae* is the hornwort species that has been suggested as a model and the chloroplast genome of this species has been sequenced [19]. To date, however, very little comparative work has been carried out with hornworts.

Lycophyte models are even less well defined than bryophyte models. There are three lycophyte orders—Isoetales, Lycopodiaceae and Selaginellaceae. We have advocated *S. kraussiana* as a model, and continue to do so, but the genome of *S. moellendorfii* has been sequenced (http://selaginella.genomics.purdue.edu). Unfortunately, *S. moellendorfii* cannot be propagated sexually because megasporangia abort [20], and thus the species cannot be used for genetic studies. Species in other lycophyte orders could potentially be developed as models. *Isoetes* is a particularly interesting group of plants because it is the only extant representative of an order with a long fossil history. Many fossil representatives of the Isoetales show parallel evolution of most of the key innovations that are generally only associated with seed plants; extreme heterospory with an enclosed megaspore, wood and bipolar growth. These features suggest a life history analogous to the majority of published reports that address macroevolutionary questions by comparing developmental genetics in angiosperms and non-flowering plants: this function could have evolved within the land plants or in algal ancestors.

- **LEAFY/FLORICAULA** (LFY/FLO), the transcription factor that regulates the formation of floral meristems in *Arabidopsis thaliana* and *Antirrhinum majus*, regulates the first cell division of the zygote in the bryophyte *P. patens* [25]. Whether the ‘ancestral’ role of LFY in cell division is retained in other non-flowering plants awaits clarification. However, LFY expression patterns in ferns are different from expression patterns of the organ identity genes that are LFY targets in angiosperms and thus the relationship between the two evolved after the divergence of ferns and seed plants [26].

- **ROOT HAIR DEFECTIVE 6** (RHD6)-like transcription factors regulate the development of root hairs in *A. thaliana* and rhizoids in the bryophyte *P. patens* [27**]. If rhizoids are not homologous to root hairs, this observation suggests recruitment of an existing ‘gametophyte’ toolkit for sporophyte root hair formation, at least in the euphyllophyte lineage. As roots evolved independently in lycophytes and euphyllophytes, it will be interesting to determine whether there was a parallel recruitment of the RHD6 pathway in lycophyte roots.

- The interaction between KNOTTED1-like homeobox (KNOX) and ARP transcription factors in the vegetative shoot apex regulates leaf development in both the lycophyte *Selaginella kraussiana* [28] and at least three euphyllophytes (*A. thaliana* [29], *Zea mays* and *A. majus* [30,31]). Additionally, ectopic expression of lycophyte (unpublished data) and fern [32] KNOX genes in angiosperm leaves, gives equivalent phenotypes to overexpression of the respective angiosperm genes. As leaves evolved independently in lycophytes and euphyllophytes, these observations suggest that the same pathway was recruited on two separate occasions and that there is a developmental constraint on how leaves can form. However, HD-ZIP proteins have different expression patterns in leaves of lycophytes and euphyllophytes [33*]. These patterns are consistent with a role in regulating the distinct vascularization patterns seen in the two groups and thus once leaf primordia are initiated, different developmental mechanisms may pattern the final form.

- The activity of KNOX proteins in angiosperms has been shown to influence, and/or be influenced by a number of hormones—namely gibberellin, cytokinin and auxin (reviewed in [34]). To date, there have been very few studies on hormone signalling in non-seed plants. However, it is interesting to note that bryophyte (*P. patens*) [35*] and fern [32] KNOX proteins function in the sporophyte but not the gametophyte and that although auxin plays a role in the gametophyte, polar auxin transport has been reported to be
sporophyte-specific in *P. patens* [36]. As auxin plays a pivotal signalling role in regulating the pattern of leaf initiation in angiosperms [37,38], these observations raise the question of whether specific KNOX/auxin interactions co-evolved in the sporophyte.

- Physical interactions between gibberellin (GA), GA receptors (GIDs), and DELLA signalling proteins are conserved in lycophytes and angiosperms, but not in *P. patens* [39,40][**,41]. However, the role of these interactions in regulating growth is not conserved in either lycophytes or *P. patens*, suggesting a step-wise recruitment of GA-mediated growth patterning during land plant evolution.

**Conclusions**

The examples outlined above illustrate how little we know about how land plant form evolved. More significant advances require the development of forward and reverse genetic technologies in non-flowering plants, and the generation of sequence data from diverse plant groups. In this regard, the recent advent of affordable parallel sequencing methods will have a big impact on the field. There are certainly plenty of questions to be answered and for those willing to work with non-model species, there are exciting challenges ahead.

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**References and recommended reading**

Papers of particular interest, published within the annual period of review, have been highlighted as:

- of special interest
- of outstanding interest


15. Prusinkiewicz P, Erasmus Y, Lane B, Harder LD, Coen E: • Evolution and development of inflorescence architectures. Science 2007, 316:1452-1456. Shows how a combination of developmental genetics and mathematical modelling can be used to predict particular morphologies and to illustrate why certain developmental transitions may be constrained.


rhizoids are present on the gametophyte and root hairs on the sporophyte, this work demonstrates that the same pathway was recruited independently for the formation of non-homologous structures.


